RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/541,626A

Source: TFWO

Date Processed by STIC: 6/14/06

ENTERED

IFWO

RAW SEQUENCE LISTING   DATE: 06/14/2006
PATENT APPLICATION: US/10/541,626A   TIME: 09:20:39

Input Set : A:\2006-06-05 0760-0347PUS1.ST25.txt
Output Set: N:\CRF4\06142006\J541626A.raw

```
 3 <110> APPLICANT: Haruo HANAWA
 5 <120> TITLE OF INVENTION: VECTOR FOR GENE THERAPY AND METHOD OF QUANTIFYING TARGET
 6       PROTEIN IN MAMMAL OR CULTURED CELLS WITH THE ADMINISTRATION
 7       OF THE VECTOR FOR GENE THERAPY
 9 <130> FILE REFERENCE: 0760-0347PUS1
11 <140> CURRENT APPLICATION NUMBER: US 10/541,626A
12 <141> CURRENT FILING DATE: 2005-07-07
14 <150> PRIOR APPLICATION NUMBER: PCT/JP2003/016956
15 <151> PRIOR FILING DATE: 2003-12-26
17 <150> PRIOR APPLICATION NUMBER: JP 2003-3967
18 <151> PRIOR FILING DATE: 2003-01-10
20 <160> NUMBER OF SEQ ID NOS: 24
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 11
24 <212> TYPE: PRT
25 <213> ORGANISM: Artificial Sequence
27 <220> FEATURE:
28 <223> OTHER INFORMATION: oligopeptide C19-29 region of glucagon of human, mouse or rat
30 <400> SEQUENCE: 1
32 Ala Gln Asp Phe Val Gln Trp Leu Met Asn Thr
33 1               5                   10
36 <210> SEQ ID NO: 2
37 <211> LENGTH: 1471
38 <212> TYPE: DNA
39 <213> ORGANISM: Artificial Sequence
41 <220> FEATURE:
42 <223> OTHER INFORMATION: DNA insert encoding rat IFN-r receptor, rat IgG Fc region
43       and glucagon C19-29 region
46 <220> FEATURE:
47 <221> NAME/KEY: CDS
48 <222> LOCATION: (13)..(1461)
49 <223> OTHER INFORMATION: DNA insert encoding rat IFN-r receptor, rat IgG Fc region
50       and glucagon C19-29 region
52 <400> SEQUENCE: 2
53 gaattcattt aa atg att ctg ctg gtg gtc ctg atg ctg tct gcg gag atc      51
54                Met Ile Leu Leu Val Val Leu Met Leu Ser Ala Glu Ile
55                 1               5                   10
57 ggg agt gga gct ttg atg agc acc gag gat cct aag ccg ccc tcg gtg       99
58 Gly Ser Gly Ala Leu Met Ser Thr Glu Asp Pro Lys Pro Pro Ser Val
59    15               20                  25
61 cct gcg cca aca aat gtt cta att acg tcc tat gac ttg aac cct gtc      147
62 Pro Ala Pro Thr Asn Val Leu Ile Thr Ser Tyr Asp Leu Asn Pro Val
63 30               35                  40                  45
```

RAW SEQUENCE LISTING   DATE: 06/14/2006
PATENT APPLICATION: US/10/541,626A   TIME: 09:20:39

Input Set : A:\2006-06-05 0760-0347PUS1.ST25.txt
Output Set: N:\CRF4\06142006\J541626A.raw

```
 65 gta cat tgg aag cac cag aac gtg tcg cag gct gcc gtc ttc act gta      195
 66 Val His Trp Lys His Gln Asn Val Ser Gln Ala Ala Val Phe Thr Val
 67                 50                  55                  60
 69 cag gta aag atg tat cca gaa tac tgg act gat gcc tgc acc aac att      243
 70 Gln Val Lys Met Tyr Pro Glu Tyr Trp Thr Asp Ala Cys Thr Asn Ile
 71             65                  70                  75
 73 gcc cat cat tat tgt aat atc tac aaa cac att tcc tat cct gac tca      291
 74 Ala His His Tyr Cys Asn Ile Tyr Lys His Ile Ser Tyr Pro Asp Ser
 75         80                  85                  90
 77 tct gcc tgg gcc aga gtt aag gcc aag gtt gga caa aga gaa tct gcc      339
 78 Ser Ala Trp Ala Arg Val Lys Ala Lys Val Gly Gln Arg Glu Ser Ala
 79     95                  100                 105
 81 tat gcg cag tca gaa gag ttt att atg tgc cga aag ggg aag gtt gga      387
 82 Tyr Ala Gln Ser Glu Glu Phe Ile Met Cys Arg Lys Gly Lys Val Gly
 83 110                 115                 120                 125
 85 ccg cct ggc ctg gac atc gga agg aag gaa gat cag ctg att gtc cac      435
 86 Pro Pro Gly Leu Asp Ile Gly Arg Lys Glu Asp Gln Leu Ile Val His
 87                 130                 135                 140
 89 ata ttt cac cct aag gtc aat gtg agt cag gaa acc atg ttt ggt gac      483
 90 Ile Phe His Pro Lys Val Asn Val Ser Gln Glu Thr Met Phe Gly Asp
 91             145                 150                 155
 93 gga aat acc tgt tac aca ttc gac tac act gtg ttt gtg aaa cat tac      531
 94 Gly Asn Thr Cys Tyr Thr Phe Asp Tyr Thr Val Phe Val Lys His Tyr
 95             160                 165                 170
 97 agg agt ggg gag atc cta cat aca gaa cat agc gtc cta aaa gaa gat      579
 98 Arg Ser Gly Glu Ile Leu His Thr Glu His Ser Val Leu Lys Glu Asp
 99     175                 180                 185
101 tgt agc gaa act ctg tgt gag tta aac atc tca gtg tcc acg ctg aat      627
102 Cys Ser Glu Thr Leu Cys Glu Leu Asn Ile Ser Val Ser Thr Leu Asn
103 190                 195                 200                 205
105 tcc aat tac tgt gtt tca gta gtt gga aag tcg tct ttc tgg caa gtt      675
106 Ser Asn Tyr Cys Val Ser Val Val Gly Lys Ser Ser Phe Trp Gln Val
107                 210                 215                 220
109 aat aca gaa aca tca aaa gac gcc tgt atc ccc ttt ctc cat gat gac      723
110 Asn Thr Glu Thr Ser Lys Asp Ala Cys Ile Pro Phe Leu His Asp Asp
111             225                 230                 235
113 aga gaa gaa gcg gcc gcc gtg ccc aga aac tgt gga ggt gat tgc aag      771
114 Arg Glu Glu Ala Ala Ala Val Pro Arg Asn Cys Gly Gly Asp Cys Lys
115             240                 245                 250
117 cct tgt ata tgt aca ggc tca gaa gta tca tct gtc ttc atc ttc ccc      819
118 Pro Cys Ile Cys Thr Gly Ser Glu Val Ser Ser Val Phe Ile Phe Pro
119     255                 260                 265
121 cca aag ccc aaa gat gtg ctc acc atc act ctg act cct aag gtc acg      867
122 Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys Val Thr
123 270                 275                 280                 285
125 tgt gtt gtg gta gac att agc cag gac gat ccc gag gtc cat ttc agc      915
126 Cys Val Val Val Asp Ile Ser Gln Asp Asp Pro Glu Val His Phe Ser
127                 290                 295                 300
129 tgg ttt gta gat gac gtg gaa gtc cac aca gct cag act cga cca cca      963
```

```
130 Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr Arg Pro Pro
131         305             310             315
133 gag gag cag ttc aac agc act ttc cgc tca gtc agt gaa ctc ccc atc   1011
134 Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu Pro Ile
135         320             325             330
137 ctg cac cag gac tgg ctc aat ggc agg acg ttc aga tgc aag gtc acc   1059
138 Leu His Gln Asp Trp Leu Asn Gly Arg Thr Phe Arg Cys Lys Val Thr
139     335             340             345
141 agt gca gct ttc cca tcc ccc atc gag aaa acc atc tcc aaa ccc gaa   1107
142 Ser Ala Ala Phe Pro Ser Pro Ile Glu Lys Thr Ile Ser Lys Pro Glu
143 350             355             360             365
145 ggc aga aca caa gtt ccg cat gta tac acc atg tca cct acc aag gaa   1155
146 Gly Arg Thr Gln Val Pro His Val Tyr Thr Met Ser Pro Thr Lys Glu
147             370             375             380
149 gag atg acc cag aat gaa gtc agt atc acc tgc atg gta aaa ggc ttc   1203
150 Glu Met Thr Gln Asn Glu Val Ser Ile Thr Cys Met Val Lys Gly Phe
151         385             390             395
153 tat ccc cca gac att tat gtg gag tgg cag atg aac ggg cag cca cag   1251
154 Tyr Pro Pro Asp Ile Tyr Val Glu Trp Gln Met Asn Gly Gln Pro Gln
155         400             405             410
157 gaa aac tac aag aac act cca cct acg atg gac aca gat ggg agt tac   1299
158 Glu Asn Tyr Lys Asn Thr Pro Pro Thr Met Asp Thr Asp Gly Ser Tyr
159     415             420             425
161 ttc ctc tac agc aag ctc aat gtg aag aag gaa aaa tgg cag cag gga   1347
162 Phe Leu Tyr Ser Lys Leu Asn Val Lys Lys Glu Lys Trp Gln Gln Gly
163 430             435             440             445
165 aac acg ttc acg tgt tct gtg ctg cat gaa ggc ctg cac aac cac cat   1395
166 Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn His His
167             450             455             460
169 act gag aag agt ctc tcc cac tct ccg ggt aaa gcc caa gat ttt gtg   1443
170 Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys Ala Gln Asp Phe Val
171         465             470             475
173 cag tgg ttg atg aat acc tgagaattct                                1471
174 Gln Trp Leu Met Asn Thr
175         480
178 <210> SEQ ID NO: 3
179 <211> LENGTH: 4790
180 <212> TYPE: DNA
181 <213> ORGANISM: Artificial Sequence
183 <220> FEATURE:
184 <223> OTHER INFORMATION: DNA sequence of artificial expression vector pCAGGS
186 <400> SEQUENCE: 3
187 gtcgacattg attattgact agttattaat agtaatcaat tacggggtca ttagttcata    60
189 gcccatatat ggagttccgc gttacataac ttacggtaaa tggcccgcct ggctgaccgc   120
191 ccaacgaccc ccgcccattg acgtcaataa tgacgtatgt tcccatagta acgccaatag   180
193 ggactttcca ttgacgtcaa tgggtggact atttacggta aactgcccac ttggcagtac   240
195 atcaagtgta tcatatgcca agtacgcccc ctattgacgt caatgacggt aaatggcccg   300
197 cctggcatta tgcccagtac atgaccttat gggactttcc tacttggcag tacatctacg   360
199 tattagtcat cgctattacc atgggtcgag gtgagcccca cgttctgctt cactctcccc   420
```

```
201 atctcccccc cctcccccacc cccaattttg tatttattta ttttttaatt attttgtgca    480
203 gcgatggggg cgggggggg ggggggcgcgc gccaggcggg gcggggcggg gcgaggggcg    540
205 gggcggggcg aggcggagag gtgcggcggc agccaatcag agcggcgcgc tccgaaagtt    600
207 tccttttatg gcgaggcggc ggcggcggcg gccctataaa aagcgaagcg cgcggcgggc    660
209 gggagtcgct gcgttgcctt cgccccgtgc cccgctccgc gccgcctcgc gccgcccgcc    720
211 ccggctctga ctgaccgcgt tactcccaca ggtgagcggg cgggacggcc cttctcctcc    780
213 gggctgtaat tagcgcttgg tttaatgacg gctcgtttct tttctgtggc tgcgtgaaag    840
215 ccttaaaggg ctccgggagg gccctttgtg cggggggggag cggctcgggg ggtgcgtgcg    900
217 tgtgtgtgtg cgtggggagc gccgcgtgcg gcccgcgctg cccggcggct gtgagcgctg    960
219 cgggcgcggc gcggggcttt gtgcgctccg cgtgtgcgcg aggggagcgc ggccggggggc   1020
221 ggtgccccgc ggtgcggggg ggctgcgagg ggaacaaagg ctgcgtgcgg ggtgtgtgcg   1080
223 tgggggggtg agcagggggt gtgggcgcgg cggtcgggct gtaacccccc cctgcacccc   1140
225 cctccccgag ttgctgagca cggcccggct tcgggtgcgg ggctccgtgc ggggcgtggc   1200
227 gcggggctcg ccgtgccggg cggggggtgg cggcaggtgg gggtgccggg cggggcgggg   1260
229 ccgcctcggg ccggggaggg ctcggggggag gggcgcggcg gccccggagc gccggcggct   1320
231 gtcgaggcgc ggcgagccgc agccattgcc ttttatggta atcgtgcgag agggcgcagg   1380
233 gacttccttt gtcccaaatc tggcggagcc gaaatctggg aggcgccgcc gcaccccctc   1440
235 tagcgggcgc gggcgaagcg gtgcggcgcc ggcaggaagg aaatgggcgg ggagggcctt   1500
237 cgtgcgtcgc cgcgccgccg tcccccttctc catctccagc ctcggggctg ccgcaggggg   1560
239 acggctgcct tcggggggga cggggcaggg cggggttcgg cttctggcgt gtgaccggcg   1620
241 gctctagagc ctctgctaac catgttcatg ccttcttctt tttcctacag ctcctgggca   1680
243 acgtgctggt tgttgtgctg tctcatcatt ttggcaaaga attcctcgag gaattcactc   1740
245 ctcaggtgca ggctgcctat cagaaggtgg tggctggtgt ggccaatgcc ctggctcaca   1800
247 aataccactg agatcttttt ccctctgcca aaaattatgg ggacatcatg aagccccttg   1860
249 agcatctgac ttctggctaa taaaggaaat ttattttcat tgcaatagtg tgttggaatt   1920
251 ttttgtgtct ctcactcgga aggacatatg ggagggcaaa tcatttaaaa catcagaatg   1980
253 agtatttggt ttagagtttg gcaacatatg ccatatgctg gctgccatga acaaaggtgg   2040
255 ctataaagag gtcatcagta tatgaaacag ccccctgctg tccattcctt attccataga   2100
257 aaagccttga cttgaggtta gatttttttt atattttgtt ttgtgttatt tttttcttta   2160
259 acatccctaa aattttcctt acatgttttta ctagccagat ttttcctcct ctcctgacta   2220
261 ctcccagtca tagctgtccc tcttctctta tgaagatccc tcgacctgca gcccaagctt   2280
263 ggcgtaatca tggtcatagc tgtttcctgt gtgaaattgt tatccgctca caattccaca   2340
265 caacatacga gccggaagca taaagtgtaa agcctggggt gcctaatgag tgagctaact   2400
267 cacattaatt gcgttgcgct cactgcccgc tttccagtcg ggaaacctgt cgtgccagcg   2460
269 gatccgcatc tcaattagtc agcaaccata gtcccgcccc taactccgcc catcccgccc   2520
271 ctaactccgc ccagttccgc ccattctccg ccccatggct gactaatttt ttttatttat   2580
273 gcagaggccg aggccgcctc ggcctctgag ctattccaga agtagtgagg aggcttttttt  2640
275 ggaggcctag gcttttgcaa aaagctaact tgtttattgc agcttataat ggttacaaat   2700
277 aaagcaatag catcacaaat ttcacaaata aagcatttt ttcactgcat tctagttgtg   2760
279 gtttgtccaa actcatcaat gtatcttatc atgtctggat ccgctgcatt aatgaatcgg   2820
281 ccaacgcgcg gggagaggcg gtttgcgtat tgggcgctct tccgcttcct cgctcactga   2880
283 ctcgctgcgc tcggtcgttc ggctgcggcg agcggtatca gctcactcaa aggcggtaat   2940
285 acggttatcc acagaatcag gggataacgc aggaaagaac atgtgagcaa aaggccagca   3000
287 aaaggccagg aaccgtaaaa aggccgcgtt gctggcgttt ttccataggc tccgcccccc   3060
289 tgacgagcat cacaaaaatc gacgctcaag tcagaggtgg cgaaacccga caggactata   3120
291 aagataccag gcgtttcccc ctggaagctc cctcgtgcgc tctcctgttc cgaccctgcc   3180
293 gcttaccgga tacctgtccg cctttctccc ttcgggaagc gtggcgcttt ctcaatgctc   3240
295 acgctgtagg tatctcagtt cggtgtaggt cgttcgctcc aagctgggct gtgtgcacga   3300
297 acccccgtt cagcccgacc gctgcgcctt atccggtaac tatcgtcttg agtccaaccc   3360
```

RAW SEQUENCE LISTING   DATE: 06/14/2006
PATENT APPLICATION: US/10/541,626A   TIME: 09:20:39

Input Set : A:\2006-06-05 0760-0347PUS1.ST25.txt
Output Set: N:\CRF4\06142006\J541626A.raw

```
299 ggtaagacac gacttatcgc cactggcagc agccactggt aacaggatta gcagagcgag   3420
301 gtatgtaggc ggtgctacag agttcttgaa gtggtggcct aactacggct acactagaag   3480
303 gacagtattt ggtatctgcg ctctgctgaa gccagttacc ttcggaaaaa gagttggtag   3540
305 ctcttgatcc ggcaaacaaa ccaccgctgg tagcggtggt ttttttgttt gcaagcagca   3600
307 gattacgcgc agaaaaaaag gatctcaaga agatcctttg atcttttcta cggggtctga   3660
309 cgctcagtgg aacgaaaact cacgttaagg gattttggtc atgagattat caaaaaggat   3720
311 cttcacctag atccttttaa attaaaaatg aagttttaaa tcaatctaaa gtatatatga   3780
313 gtaaacttgg tctgacagtt accaatgctt aatcagtgag gcacctatct cagcgatctg   3840
315 tctatttcgt tcatccatag ttgcctgact ccccgtcgtg tagataacta cgatacggga   3900
317 gggcttacca tctggcccca gtgctgcaat gataccgcga gacccacgct caccggctcc   3960
319 agatttatca gcaataaacc agccagccgg aagggccgag cgcagaagtg gtcctgcaac   4020
321 tttatccgcc tccatccagt ctattaattg ttgccgggaa gctagagtaa gtagttcgcc   4080
323 agttaatagt ttgcgcaacg ttgttgccat tgctacaggc atcgtggtgt cacgctcgtc   4140
325 gtttggtatg gcttcattca gctccggttc ccaacgatca aggcgagtta catgatcccc   4200
327 catgttgtgc aaaaaagcgg ttagctcctt cggtcctccg atcgttgtca gaagtaagtt   4260
329 ggccgcagtg ttatcactca tggttatggc agcactgcat aattctctta ctgtcatgcc   4320
331 atccgtaaga tgcttttctg tgactggtga gtactcaacc aagtcattct gagaatagtg   4380
333 tatgcggcga ccgagttgct cttgcccggc gtcaatacgg gataataccg cgccacatag   4440
335 cagaacttta aaagtgctca tcattggaaa acgttcttcg gggcgaaaac tctcaaggat   4500
337 cttaccgctg ttgagatcca gttcgatgta acccactcgt gcacccaact gatcttcagc   4560
339 atcttttact ttcaccagcg tttctgggtg agcaaaaaca ggaaggcaaa atgccgcaaa   4620
341 aaagggaata agggcgacac ggaaatgttg aatactcata ctcttccttt ttcaatatta   4680
343 ttgaagcatt tatcagggtt attgtctcat gagcggatac atatttgaat gtatttagaa   4740
345 aaataaacaa atagggggttc cgcgcacatt tccccgaaaa gtgccacctg              4790
```

348 <210> SEQ ID NO: 4
349 <211> LENGTH: 1233
350 <212> TYPE: DNA
351 <213> ORGANISM: Artificial Sequence
353 <220> FEATURE:
354 <223> OTHER INFORMATION: DNA insert encoding rat CTLA4, rat IgG Fc region and
355   glucagon C19-29 region
357 <220> FEATURE:
358 <221> NAME/KEY: CDS
359 <222> LOCATION: (13)..(1224)
360 <223> OTHER INFORMATION: DNA insert encoding rat CTLA4, rat IgG Fc region and
361   glucagon C19-29 region
363 <400> SEQUENCE: 4

```
364 gaattcattt aa atg gct tgt ctt gga ctc cag agg tac aaa act cac ctg    51
365               Met Ala Cys Leu Gly Leu Gln Arg Tyr Lys Thr His Leu
366                1               5                   10
368 cag ctg cct tct agg act tgg cct ttt gga gtc ctg ctt tct ctt ctc      99
369 Gln Leu Pro Ser Arg Thr Trp Pro Phe Gly Val Leu Leu Ser Leu Leu
370     15                  20                  25
372 ttc atc cca atc ttc tct gaa gcc ata caa gtg acc caa cct tca gtg     147
373 Phe Ile Pro Ile Phe Ser Glu Ala Ile Gln Val Thr Gln Pro Ser Val
374 30                  35                  40                  45
376 gtg ttg gcc agc agc cac ggt gtc gcc agc ttt cca tgt gaa tat gca     195
377 Val Leu Ala Ser Ser His Gly Val Ala Ser Phe Pro Cys Glu Tyr Ala
378                 50                  55                  60
```

VERIFICATION SUMMARY   DATE: 06/14/2006
PATENT APPLICATION: **US/10/541,626A**   TIME: 09:20:40

Input Set : **A:\2006-06-05 0760-0347PUS1.ST25.txt**
Output Set: **N:\CRF4\06142006\J541626A.raw**